

Amendments to the Specification

At the indicated page and line numbers, please replace the existing paragraphs with the ones set forth below.

(Page 7, line 29 through page 8, line 5)

(i) Novel, naturally occurring, nucleic acids, isolatable using the sequences of the present invention. They may include alleles (which will include polymorphisms or mutations at one or more bases - for instance vrn1-1 (SEQ ID NO: 12) or vrn1-2 (SEQ ID NO: 13) shown in Fig 7) or pseudoalleles (which may occur at closely linked loci to the VRN1 gene). Also included are paralogues, isogenes, or other homologous genes belonging to the same family as the VRN1 gene. Although these may occur at different genomic loci to the gene, they are likely to share conserved regions with it (see e.g. RTV1 in the Examples below). Also included are homologues of VRN1 from other plant species.

(Page 36, lines 15-16)

Fig 6: Structure of the VRN1 gene and transcript, and positions of the vrn1-1 and vrn1-2 mutations. SEQ ID NOs: 2 and 3 (top) and SEQ ID NOs: 4 and 5 (bottom) are shown in the nonsense mutation box and SEQ ID NOs: 6 and 7 (top) and SEQ ID NOs: 8 and 9 (bottom) are shown in the 1 bp deletion/frameshift mutation box.

(Page 36, lines 18-19)

Fig 7: The putative VRN1 transcript and its deduced amino acid sequence (SEQ ID NO: 10; the amino acid sequence is SEQ ID NO: 11).

(Page 36, line 21)

Fig 8: Alignment of VRN1 (SEQ ID NO: 11) and RTV1 (SEQ ID NO: 48).

(Page 40, line 21 through page 41, line 14)

Eight cosmids (39K3, 8H8, 10F10, 42A10, 2P5, 19D3, 27J7, 67N6) centered around the marker *agp14* were transformed into *vrn1-1 fca-1* plants by *Agrobacterium tumefaciens*-infection of root tissue (Hooykaas, 1989). In order to test if any of these cosmids rescued the mutant phenotype of *vrn1-1 fca-1*, T2 seed (from individual T1 kanamycin resistant transformants) was sown on soil and vernalized for 5 weeks. Seedlings were then transferred to LD conditions, and pricked out into individual compartments of divided trays after about a week of growth. The total leaf number prior to flowering was determined, and cosmids were scored as complementing if the segregation ratio of early to late plants (compared to *fca-1* and *vrn1-1 fca-1* controls) was approximately 3:1 or greater. Eight independent lines containing cosmid 8H8, eight independent lines containing cosmid 10F10, and three independent lines containing cosmid 39K3 were found to rescue mutant phenotype of *vrn1-1 fca-1*. Lines containing the other five cosmids did not complement the *vrn1-1* phenotype (Figure 3). Analysis of the flowering time segregation in typical 8H8 and 10F10 complementing lines is shown in Figure 4. The presence of each cosmid in complementing lines (T2 plants) was confirmed by a cosmid-specific diagnostic PCR, comprising an insert specific primer 8H8DIAG1 (ACCTGCTTCTGCCAACCGCTC; SEQ ID NO: 14) and 10F10DIAG1 (AGTCGCTCTGCTGTTTTTCCC; SEQ ID NO: 15) (corresponding to a portion of the Ler genomic DNA) and a primer BACT 7U (CCTCTTCGCTATTACGCCAG; SEQ ID NO: 16) present in the cosmid vector (see "cosmid complementation" under "materials and methods" below).

(Page 55, lines 1-4)

| | | |
|--------|--------------------------------|------------------------|
| BACT7U | 5' - CCTCTTCGCTATTACGCCAG -3' | <u>(SEQ ID NO: 16)</u> |
| BACT7L | 5' - GCCCTTCCCAACAGTCG -3' | <u>(SEQ ID NO: 17)</u> |
| Sp6A | 5' - CACACAGGAAACAGCTAT -3' | <u>(SEQ ID NO: 18)</u> |
| Sp6B | 5' - ACACAAACATACGAGCCGGAA -3' | <u>(SEQ ID NO: 19)</u> |

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| Oligo | Strand | Position | Sequence (5' to 3') | (SEQ ID NO:) |
|-------|--------|----------|-----------------------|-----------------|
| S63 | + | 850 | CAACGGTTAGCCCCAAC | (SEQ ID NO: 20) |
| S64 | - | 866 | GTTTGGGCTAACCGTTG | (SEQ ID NO: 21) |
| V11 | + | 1193 | GAGACCAGTTTGTTC | (SEQ ID NO: 22) |
| S62 | - | 1229 | GACAAATATAAGGTGGAAAGG | (SEQ ID NO: 23) |
| S66 | + | 1441 | AAAGGGGAGTAGGTGGG | (SEQ ID NO: 24) |
| V7 | + | 1811 | CTCTCTGGTCTTCTCTC | (SEQ ID NO: 25) |
| V10 | - | 1828 | GAAGAGAAGACCAGAGAG | (SEQ ID NO: 26) |
| V6 | + | 1907 | TTTTCTCATCCACTATCC | (SEQ ID NO: 27) |
| S51 | - | 1930 | TTTCTTGGATAGTGGATGAG | (SEQ ID NO: 28) |
| S65 | - | 2166 | AAAACAGGGAAGAGTAAGAAG | (SEQ ID NO: 29) |
| S52 | + | 2270 | CATTGGTTGTGTTGGTGGG | (SEQ ID NO: 30) |
| V5 | + | 2599 | GGTCTCTATGTATTGTGC | (SEQ ID NO: 31) |
| V4 | - | 2616 | GCACAATACATAGAGACC | (SEQ ID NO: 32) |
| V12 | - | 2846 | AGATTGATTACACGACTCC | (SEQ ID NO: 33) |
| V8 | + | 3125 | CCCAGATAAGTTGTGAG | (SEQ ID NO: 34) |
| V3 | + | 3391 | ATTCCGCTCACACCAC | (SEQ ID NO: 35) |
| V15 | - | 3414 | GTGGAAGTGGTTGTGAG | (SEQ ID NO: 36) |
| V14 | + | 3477 | TACCCATCACCACTTCC | (SEQ ID NO: 37) |
| S60 | - | 3474 | CAGAAGAAGGAAAGATGACC | (SEQ ID NO: 38) |
| S61 | + | 3927 | GAAGAAAGAGAGAGAGCC | (SEQ ID NO: 39) |
| V13 | + | 3976 | ACCCTTCTTCAGAGTG | (SEQ ID NO: 40) |
| V9 | - | 3942 | CTCTCTCTCTTCTCTG | (SEQ ID NO: 41) |
| V16 | - | 3993 | CCACTCTGAAGAAAGGG | (SEQ ID NO: 42) |
| S46 | + | 4096 | CCTTCTGTTCTGTTCTC | (SEQ ID NO: 43) |
| S45 | - | 4114 | GAGAACAGAACAGAAGG | (SEQ ID NO: 44) |
| V2 | - | 4431 | AAGATACTCCTACACGAC | (SEQ ID NO: 45) |
| V17 | + | 4486 | GTCTCGTTTTCTCTCGG | (SEQ ID NO: 46) |
| S49 | - | 4870 | CTACCACAGTTCCCACCTAC | (SEQ ID NO: 47) |

(Page 70, line 1)

Annex I - Ler VRN1 genomic (contig 29 [1501-6500]) (SEQ ID NO:
1)